

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: US-09-540-235-1
March 2, 2002, 20:28:56 ; Search time 2699.18 Seconds
(without alignments)
2649.239 Million cell updates/sec

Title: Perfect score: 408

Sequence: 1.acggcgtcgttggaaatta.....acatccatctaattgttgttta 408

Scoring table: IDENTITY_NUC
gapext 10.0 , Gapext 1.0

Searched: 17159718 seqs, 8763200856 residues

Total number of hits satisfying chosen parameters: 34319436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Parents_NA_Main:*

```

1: /cgn2_6/ptodata/1/pna/PCUTS_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US092_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US093_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US098_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US099_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US600_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US601_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US603_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US604_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US605_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US606_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US607_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US608_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US609_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US610_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	408	100.0	408	Sequence 1, Appli
2	408	100.0	408	Sequence 2, Appli
3	302.4	74.1	384	Sequence 4188, Ap
4	302.4	74.1	417	Sequence 5042, Ap
5	235.2	57.6	298	Sequence 4189, Ap
6	235.2	57.6	417	Sequence 5043, Ap
7	133.2	562	32.4	Sequence 388, Ap
8	132.8	32.5	371	Sequence 18213, A
9	132.8	32.5	23	Sequence 36933, A
10	132.8	32.5	384	Sequence 09-411-999-3936
11	132.8	32.5	23	Sequence 09-605-701-5338
12	132.8	32.5	429	Sequence 11618, A
13	132.8	32.5	471	Sequence 09-605-701-6552
14	132.8	32.5	23	Sequence 09-605-701-5558
15	132.8	32.5	497	Sequence 150388, Ap
16	132.8	32.5	543	Sequence 3216, A
17	132.8	32.5	555	Sequence 17346, A
18	132.8	32.5	23	Sequence 17346, A
19	132.8	32.5	58	Sequence 2434, A
20	132.8	32.5	946	Sequence 1929, A
21	130	31.9	31	Sequence 09-867-116-19329
22	130	31.9	417	Sequence 150388, Ap
23	130	31.9	27	Sequence 09-684-116-150388
24	130	31.9	449	Sequence 17346, A
25	130	31.9	22	Sequence 17346, A
26	130	31.9	666	Sequence 56964, A
27	130	31.9	58	Sequence 229237, A
28	130	31.9	724	Sequence 127760, A
29	130	31.9	25	Sequence 09-654-816-27760
30	130	31.9	724	Sequence 127760, A
31	129	31.6	51860	Sequence 980, Ap
32	129	31.6	20	Sequence 09-534-859-980
33	126	30.9	31	Sequence 09-803-736-980
34	124.2	30.4	370	Sequence 31113, A
35	124.2	30.4	27	Sequence 09-724-750-23275
36	124.2	30.4	370	Sequence 23275, A
37	124.2	30.4	50	Sequence 2416, A
38	124.2	30.4	432	Sequence 165221, A
39	124.2	30.4	27	Sequence 09-684-116-165221
40	124.2	30.4	439	Sequence 165221, A
41	124.2	30.4	25	Sequence 09-654-617-153103
42	124.2	30.4	469	Sequence 153103, A
43	124.2	30.4	473	Sequence 153505, A
44	124.2	30.4	475	Sequence 161426, A

RESULT 5
US 60-128-439-4189
Sequence 4189, Application US/60128439
GENERAL INFORMATION:
APPLICANT: Fisher, Dane K.
APPLICANT: Lalguddi, Raghunath V.
TITLE OF INVENTION: Nucleic Acid Sequences from Cyanidium caldarium and uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 38-21(15749)A
CURRENT APPLICATION NUMBER: US/60/128, 439
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 5661
SEQ ID NO 4189
LENGTH: 298
TYPE: DNA
ORGANISM: Cyanidium caldarium
FEATURE:
OTHER INFORMATION: Clone ID: LIB190-054-Q1-E1-D12
US-60-128-439-4189

FILE REFERENCE: 11000.1041U3
 CURRENT APPLICATION NUMBER: US/09/605,701
 CURRENT FILING DATE: 2000-06-21
 NUMBER OF SEQ ID NOS: 25120
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4652
 LENGTH: 471
 TYPE: DNA
 ORGANISM: Pinus radiata
 US-09-605-701-4652

Query Match 32.5%; Score 132.8; DB 23; Length 471;
 Best Local Similarity 63.4%; Pred. No. 1.4e-29; DB 203;
 Matches 0; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 88 cagtgcggcgcgaaaggattccaaatgttgtatcgctcgatcgaaaggaaatcgat 147

Db 78 cattcaggatggatcacaatccaaatcgactcgatccaggaaaggccgcggac 137

Qy 148 acttcaagacaccatcttgcgtggatcactatcgatggccgcgttgcggat 207

Db 138 atttcaactgcgcacatcttagtgcgtgcgcgtttatgtatcgatccggat 197

Qy 208 tacgtacgaaatacagcgctcgatccatcttgcgttgcgtatcgatccatcg 267

Db 198 tggaaacaatcgatgttgcgttcgcattatggatggatgtatcgatccgg 257

Qy 268 ttccgcgagtttccaggtagatggaaaggaaatcgatccaaatcgatccatcg 327

Db 258 tacgaggaaatccatcgatggatggatggatggatcgatccatcgatccgg 317

Qy 328 ggatcatatcgatggatggatggatggatgtatcgatccatcgatccatcg 387

Db 318 tcatatcgatgttgcgtatctcgatcgatggaaatcgatccatcgatccatcg 377

Qy 318 tacatccatcgatgtgt 407

Db 378 tccacccatccaaaggcggt 397

RESULT 13

US-09-606-755-858, Application US/09606755

; GENERAL INFORMATION:
 ; APPLICANT: Havukka, Ilkka

; APPLICANT: Shenk, Michael A.

; TITLE OF INVENTION: Polynucleotides isolated from plants and

; TITLE OF INVENTION: methods for their use.

; FILE REFERENCE: 1023U
 ; CURRENT APPLICATION NUMBER: US/09/411,999

; CURRENT FILING DATE: 1999-10-04
 ; NUMBER OF SEQ ID NOS: 3,897

; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 32416

; LENGTH: 543
 ; TYPE: DNA
 ; ORGANISM: Pinus radiata
 ; US-09-411-999-32416

Query Match 32.5%; Score 132.8; DB 18; Length 543;
 Best Local Similarity 63.4%; Pred. No. 1.4e-29; DB 203;
 Matches 0; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 88 cagtgcggcgcgaaaggattccaaatgttgtatcgatcgatcgaaaggaaatcgat 147

Db 71 cattcaggatggatcacaatccaaatcgactcgatccaggaaaggccgcggac 130

Qy 148 acttcaagacaccatcttgcgtggatcactatcgatggccgcgttgcggat 207

Db 131 atttcaactgcgcacatcttagtgcgtgcgcgtttatgtatcgatccggat 190

Qy 208 tacgtacgaaatacagcgctcgatccatcttgcgttgcgtatcgatccatcg 267

Db 191 tggaaacaatcgatgttgcgttcgcattatggatggatgtatcgatccgg 250

Qy 268 ttccgcgagtttccaggtagatggaaaggaaatcgatccaaatcgatccatcg 327

Db 251 tacgaggaaatccatcgatggatggatggatgtatcgatccatcgatccgg 310

Qy 328 ggatcatatcgatggatggatggatgtatcgatccatcgatccatcgatcc 387

Db 311 tcatatcgatgttgcgtatctcgatcgatggaaatcgatccatcgatccatcg 370

RESULT 15

US-09-605-701-17385

; Sequence 17385, Application US/09605701

; GENERAL INFORMATION:
 ; APPLICANT: Havukka, Ilkka

; APPLICANT: Shenk, Michael A.

; TITLE OF INVENTION: Polynucleotides, Material Incorporating

Qy 208 tacgtacgaaatacagcgctcgatccatcttgcgttgcgtatcgatccatcg 267
 Db 146 tggaaacaatcgatgttgcgttcgcattatggatgtatcgatccggat 205
 Qy 268 ttccgcgagtttccaggtagatggaaaggaaatcgatccaaatcgatccatcg 327
 Db 206 tacgaggaaatcgatgttgcgttcgcattatggatgtatcgatccggat 265
 Qy 328 ggatcatatcgatggatggatgtatcgatccatcgatccatcgatccatcg 387
 Db 266 tcatatcgatgttgcgtatctcgatcgatggaaatcgatccatcgatccatcg 325
 Qy 388 tacatccatcgatgtgt 407
 Db 326 tccacccatccaaaggcggt 345

TITLE OF INVENTION: Them, and Methods for Using Them
FILE REFERENCE: 111000-0141U3
CURRENT APPLICATION NUMBER: US/09/605,701
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NO: 25120
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17385
LENGTH: 555
TYPE: DNA
ORGANISM: *Pinus radiata*
-09-605-701-17385

Search completed: March 2, 2002, 23:02:24
Job time: 9208 sec

